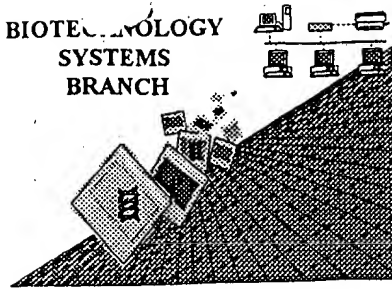


O K. Carlson

BIOTECHNOLOGY
SYSTEMS
BRANCH



P#10

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/445,362
Source: 1653
Date Processed by STIC: 4-17-01

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APR 25 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

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Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/445,362

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

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- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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p. 1

~~SEQUENCE LISTING~~ → Delete

Does Not Comply
Corrected Diskette Needed

<110> MediGene Aktiengesellschaft

<120> Myocardium- and skeletal muscle-specific nucleic acid,
its preparation and use

<150> 19725186.2

<151> June 13, 1997

move
<170> here to 5 → 5 listed, 7 shown. See p. 4

<210> 1

<211> 1936

<212> DNA

<170> FastSEQ for Windows Version 3.0

<213> Homo sapiens

<400> 1

CAGCCTGCCA	CTTGCCCTCCC	TGCCTGCTTC	TGGCTGCCTT	GAATGCCTGG	TCCTTCAAGC	60
TCCTTCTGGG	TCTGACAAAG	CAGGGACCAT	GTCTACCTTT	GGCTACCGAA	GAGGACTCAG	120
TAAATACGAA	TCCATCGACG	AGGATGAACT	CCTCGCCTCC	CTGTCAGCCG	AGGAGCTGAA	180
GGAGCTAGAG	AGAGAGTTGG	AAGACATTGA	ACCTGACCGC	AACCTTCCCG	TGGGGCTAAG	240
GCAAAAGAGC	CTGACAGAGA	AAACCCCCAC	AGGGACATTC	AGCAGAGAGG	CACTGATGGC	300
CTATTGGGAA	AAGGAGTCCC	AAAAACTCTT	GGAGAAGGAG	AGGCTGGGGG	AATGTGGAAA	360
GGTTGCAGAA	GACAAAGAGG	AAAGTGAAGA	AGAGCTTATC	TTTACTGAAA	GTAACAGTGA	420
GGTTTCTGAG	GAAGTGATA	CAGAGGAGGA	GGAGGAGGAG	TCCCAGGAGG	AAGAGGAGGA	480

New sequence rules:
use lower case letters
for nucleic bases.

Note: See # 5 on the Error
Summary Sheet. The sequence
listing could not be processed.

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<210> 3

<211> 2268 2268 listed, 1650 shown

<212> DNA

<213> Homo sapiens

lower case

<400> 3

CAGCCTGCCA CTTGCCTCCC TGCCTGCTTC TGGCTGCCTT GAATGCCTGG TCCTTCAAGC 60
TCCTTCTGGG TCTGACAAAG CAGGGACCAT GTCTACCTTT GGCTACCGAA GAGGACTCAG 120
TAAATACGAA TCCATCGACG AGGATGAACT CCTCGCCTCC CTGTCAGCCG AGGAGCTGAA 180
GGAGCTAGAG AGAGAGTTGG AAGACATTGA ACCTGACCGC AACCTTCCCG TGGGGCTAAG 240
GCAAAAGAGC CTGACAGAGA AAACCCCCAC AGGGACATTC AGCAGAGAGG CACTGATGGC 300
CTATTGGGAA AAGGAGTCCC AAAAATCTTT GGAGAAGGAG AGGCTGGGGG AATGTGGAAA 360
GGTTGCAGAA GACAAAGAGG AAAGTGAAGA AGAGCTTATC TTTACTGAAA GTAACAGTGA 420
GGTTTCTGAG GAAGTGTATA CAGAGGAGGA GGAGGAGGAG TCCCAGGAGG AAGAGGAGGA 480
AGAAGACAGT GACGAAGAGG AAAGAACAAT TGAAACTGCA AAAGGGATTA ATGGAAGTGT 540
AAATTATGAT AGTGCAATT CTGACAATC TAAGCCAAAG ATATTTAAAA GTCAAATAGA 600
GAACATAAAT TTGACCAATG GCAGCAATGG GAGGAACACA GAGTCCCCAG CTGCCATTCA 660
CCCTTGTTGA AATCCTACAG TGATTGAGGA CGCTTTGGAC AAGATTAAAA GCAATGACCC 720
TGACACCACA GAAGTCAATT TGAACAACAT TGAGAACATC ACAACACAGA CCCTTACCCG 780
CTTTGCTGAA GCCCTCAAGG ACAACACTGT GGTGAAGACG TTCAGTCTGG CCAACACGCA 840
TGCCGACGAC AGTGCAGCCA TGGCCATTGC AGAGATGCTC AAAGCCAATG AGCACATCAC 900
CAACGTAAAC GTCGAGTCCA ACTTCATAAC GGGAAAGGGG ATCCTGGCCA TCATGAGAGC 960
TCTCCAGCAC AACACGGTGC TCACGGAGCT GCGTTTCCAT AACCAGAGGC ACATCATGGG 1020
CAGCCAGGTG GAAATGGAGA TTGTCAAGCT GCTGAAGGAG AACACGACGC TGCTGAGGCT 1080
GGGATACCAT TTTGAACTCC CAGGACCAAG AATGAGCATG ACGAGCATTT TGACAAGAAA 1140
TATGGATAAA CAGAGGCAAA AACGTTTGCA GGAGCAAAA CAGCAGGAGG GATACGATGG 1200
AGGACCCAAT CTTAGGACCA AAGTCTGGCA AAGAGGAACA CCTAGCTCTT CACCTTATGT 1260
ATCTCCCAGG CACTCACCCCT GGTCAATCCC AAAACTCCCC AAAAAAGTCC AGACTGTGAG 1320
GAGCCGTCCT CTGTCTCCTG TGGCCACACT TCCTCCTCCT CCCCCTCCTC CTCCTCCTCC 1380
CCCTCCTTCT TCCCAAAGGC TGCCACCACC TCCTCCTCCT CCCCCTCCTC CACTCCCAGA 1440
GAAAAAGCTC ATTACCAGAA ACATTGCAGA AGTCATCAAA CAACAGGAGA GTGCCCAACG 1500
GGCATTACAA AATGGACAAA AAAAGAAAAA AGGAAAAAAG GTCAAGAAAC AGCCAAACAG 1560
TATTCTAAAG GAAATAAAAA ATTCTCTGAG GTCAGTGCAA GAGAAGAAAA TGAAGACAG 1620
TTCCCACCT TCTACCCAC AGAGATCAGC

1650

Delete non-ascii
garbage.

Non-ascii garbage throughout the middle of the sequence listing. see #5 on the Error Summary sheet.

→ sequence listing appears to begin again.

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<400> 7

Only 5 sequences were listed in <160>

See p. 1

Pro Thr Arg Asn Pro Thr Thr Val Gln Pro Trp Ser Leu Gln Arg Cys

1 5 10 15

Ile Lys Val Asn Glu His Ile Thr Asn Val Asn Val Glu Ser Asn Phe

20 25 30

Ile Thr Gly Lys Gly Ile Leu Ala Ile Met Arg Ala Leu Gln His Asn

35 40 45

Thr Val Leu Thr Glu Leu Arg Phe His Asn Gln Arg His Ile Met Gly

50 55 60

Ser Gln Val Glu Met Glu Ile Val Lys Leu Leu Lys Glu Asn Thr Thr

65 70 75 80

Leu Leu Arg Leu Gly Tyr His Phe Lys Leu Pro Gly

85 90